



## SEQUENCE LISTING

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SEP 27 2001  
TECH CENTER 1600/2900

## (1) GENERAL INFORMATION:

(i) APPLICANT: Chandrasekharappa, Settara C.  
Guru, Siradanahalli C.  
Manickam, Pachiappan  
Collins, Francis S.  
Emmert-Buck, Michael R.  
Debelenko, Larisa V.  
Lubensky, Irina A.  
Liotta, Lance A.  
Agarwal, Sunita K.  
Spiegel, Allen M.

(ii) TITLE OF INVENTION: MEN1, the Gene Associated With Multiple  
Endocrine Neoplasia Type 1, Menin Polypeptides, and Uses  
Thereof

(iii) NUMBER OF SEQUENCES: 28

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
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(C) CITY: San Francisco  
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(E) COUNTRY: USA  
(F) ZIP: 94111-3834

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/380,337  
(B) FILING DATE: 06-MAR-2000  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/040,269  
(B) FILING DATE: 05-MAR-1997

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US98/04258  
(B) FILING DATE: 04-MAR-1998

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lockyer, Jean M.  
(B) REGISTRATION NUMBER: 44,879  
(C) REFERENCE/DOCKET NUMBER: 015280-315100US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200  
(B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 111..1940
- (D) OTHER INFORMATION: /product= "human menin"

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1..87

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 88..555

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 556..764

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 765..893

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 894..934

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 935..1022

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1023..1159

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1160..1295

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1296..1460

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1461..2764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGTCCGGA GCCGCGGACC TAGAGATCCC AGAAGCCACA GCGCAGCGGC CCGGCCCCGCC

ACTATTTCCA GGCTCTGCGG GGCAGGGGCC GCCGCCCACC GCCCGCCGCC ATG GGG 116  
 Met Gly  
 1

CTG AAG GCC GCC CAG AAG ACG CTG TTC CCG CTG CGC TCC ATC GAC GAC 164  
 Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile Asp Asp  
 5 10 15

GTG GTG CGC CTG TTT GCT GCC GAG CTG GGC CGA GAG GAG CCG GAC CTG 212  
 Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro Asp Leu  
 20 25 30

GTG CTC CTT TCC TTG GTG CTG GGC TTC GTG GAG CAT TTT CTG GCT GTC 260  
 Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu Ala Val  
 35 40 45 50

AAC CGC GTC ATC CCT ACC AAC GTT CCC GAG CTC ACC TTC CAG CCC AGC 308  
 Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln Pro Ser  
 55 60 65

CCC GCC CCC GAC CCG CCT GGC GGC CTC ACC TAC TTT CCC GTG GCC GAC 356  
 Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val Ala Asp  
 70 75 80

CTG TCT ATC ATC GCC GCC CTC TAT GCC CGC TTC ACC GCC CAG ATC CGA 404  
 Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln Ile Arg  
 85 90 95

GGC GCC GTC GAC CTG TCC CTC TAT CCT CGA GAA GGG GGT GTC TCC AGC 452  
 Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val Ser Ser  
 100 105 110

CGT GAG CTG GTG AAG AAG GTC TCC GAT GTC ATA TGG AAC AGC CTC AGC 500  
 Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser Leu Ser  
 115 120 125 130

CGC TCC TAC TTC AAG GAT CGG GCC CAC ATC CAG TCC CTC TTC AGC TTC 548  
 Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe Ser Phe  
 135 140 145

ATC ACA GGC ACC AAA TTG GAC AGC TCC GGT GTG GCC TTT GCT GTG GTT 596  
 Ile Thr Gly Thr Lys Leu Asp Ser Ser Gly Val Ala Phe Ala Val Val  
 150 155 160

GGG GCC TGC CAG GCC CTG GGT CTC CGG GAT GTC CAC CTC GCC CTG TCT 644  
 Gly Ala Cys Gln Ala Leu Gly Leu Arg Asp Val His Leu Ala Leu Ser  
 165 170 175

GAG GAT CAT GCC TGG GTA GTG TTT GGG CCC AAT GGG GAG CAG ACA GCT 692  
 Glu Asp His Ala Trp Val Val Phe Gly Pro Asn Gly Glu Gln Thr Ala  
 180 185 190

GAG GTC ACC TGG CAC GGC AAG GGC AAC GAG GAC CGC AGG GGC CAG ACA 740  
 Glu Val Thr Trp His Gly Lys Gly Asn Glu Asp Arg Arg Gly Gln Thr  
 195 200 205 210

GTC AAT GCC GGT GTG GCT GAG CGG AGC TGG CTG TAC CTG AAA GGA TCA 788  
 Val Asn Ala Gly Val Ala Glu Arg Ser Trp Leu Tyr Leu Lys Gly Ser  
 215 220 225

TAC	ATG	CGC	TGT	GAC	CGC	AAG	ATG	GAG	GTG	GCG	TTC	ATG	GTG	TGT	GCC	836
Tyr	Met	Arg	Cys	Asp	Arg	Lys	Met	Glu	Val	Ala	Phe	Met	Val	Cys	Ala	
			230					235					240			
ATC	AAC	CCT	TCC	ATT	GAC	CTG	CAC	ACC	GAC	TCG	CTG	GAG	CTT	CTG	CAG	884
Ile	Asn	Pro	Ser	Ile	Asp	Leu	His	Thr	Asp	Ser	Leu	Glu	Leu	Leu	Gln	
		245					250					255				
CTG	CAG	CAG	AAG	CTG	CTC	TGG	CTG	CTC	TAT	GAC	CTG	GGA	CAT	CTG	GAA	932
Leu	Gln	Gln	Lys	Leu	Leu	Trp	Leu	Leu	Tyr	Asp	Leu	Gly	His	Leu	Glu	
	260					265					270					
AGG	TAC	CCC	ATG	GCC	TTA	GGG	AAC	CTG	GCA	GAT	CTA	GAG	GAG	CTG	GAG	980
Arg	Tyr	Pro	Met	Ala	Leu	Gly	Asn	Leu	Ala	Asp	Leu	Glu	Glu	Leu	Glu	
	275				280					285					290	
CCC	ACC	CCT	GGC	CGG	CCA	GAC	CCA	CTC	ACC	CTC	TAC	CAC	AAG	GGC	ATT	1028
Pro	Thr	Pro	Gly	Arg	Pro	Asp	Pro	Leu	Thr	Leu	Tyr	His	Lys	Gly	Ile	
			295					300						305		
GCC	TCA	GCC	AAG	ACC	TAC	TAT	CGG	GAT	GAA	CAC	ATC	TAC	CCC	TAC	ATG	1076
Ala	Ser	Ala	Lys	Thr	Tyr	Tyr	Arg	Asp	Glu	His	Ile	Tyr	Pro	Tyr	Met	
		310					315						320			
TAC	CTG	GCT	GGC	TAC	CAC	TGT	CGC	AAC	CGC	AAT	GTG	CGG	GAA	GCC	CTG	1124
Tyr	Leu	Ala	Gly	Tyr	His	Cys	Arg	Asn	Arg	Asn	Val	Arg	Glu	Ala	Leu	
	325						330					335				
CAG	GCC	TGG	GCG	GAC	ACG	GCC	ACT	GTC	ATC	CAG	GAC	TAC	AAC	TAC	TGC	1172
Gln	Ala	Trp	Ala	Asp	Thr	Ala	Thr	Val	Ile	Gln	Asp	Tyr	Asn	Tyr	Cys	
	340					345					350					
CGG	GAA	GAC	GAG	GAG	ATC	TAC	AAG	GAG	TTC	TTT	GAA	GTA	GCC	AAT	GAT	1220
Arg	Glu	Asp	Glu	Glu	Ile	Tyr	Lys	Glu	Phe	Phe	Glu	Val	Ala	Asn	Asp	
	355				360					365					370	
GTC	ATC	CCC	AAC	CTG	CTG	AAG	GAG	GCA	GCC	AGC	TTG	CTG	GAG	GCG	GGC	1268
Val	Ile	Pro	Asn	Leu	Leu	Lys	Glu	Ala	Ala	Ser	Leu	Leu	Glu	Ala	Gly	
			375					380						385		
GAG	GAG	CGG	CCG	GGG	GAG	CAA	AGC	CAG	GGC	ACC	CAG	AGC	CAA	GGT	TCC	1316
Glu	Glu	Arg	Pro	Gly	Glu	Gln	Ser	Gln	Gly	Thr	Gln	Ser	Gln	Gly	Ser	
		390					395						400			
GCC	CTC	CAG	GAC	CCT	GAG	TGC	TTC	GCC	CAC	CTG	CTG	CGA	TTC	TAC	GAC	1364
Ala	Leu	Gln	Asp	Pro	Glu	Cys	Phe	Ala	His	Leu	Leu	Arg	Phe	Tyr	Asp	
		405				410						415				
GGC	ATC	TGC	AAA	TGG	GAG	GAG	GGC	AGT	CCC	ACG	CCT	GTG	CTG	CAC	GTG	1412
Gly	Ile	Cys	Lys	Trp	Glu	Glu	Gly	Ser	Pro	Thr	Pro	Val	Leu	His	Val	
	420					425					430					
GGC	TGG	GCC	ACC	TTT	CTT	GTG	CAG	TCC	CTA	GGC	CGT	TTT	GAG	GGA	CAG	1460
Gly	Trp	Ala	Thr	Phe	Leu	Val	Gln	Ser	Leu	Gly	Arg	Phe	Glu	Gly	Gln	
	435				440					445					450	
GTG	CGG	CAG	AAG	GTG	CGC	ATA	GTG	AGC	CGA	GAG	GCC	GAG	GCG	GCC	GAG	1508
Val	Arg	Gln	Lys	Val	Arg	Ile	Val	Ser	Arg	Glu	Ala	Glu	Ala	Ala	Glu	
			455						460					465		

GCC GAG GAG CCG TGG GGC GAG GAA GCC CGG GAA GGC CGG CGG CGG GGC	1556
Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg Gly	
470 475 480	
CCA CGG CGG GAG TCC AAG CCA GAG GAG CCC CCG CCG CCC AAG AAG CCA	1604
Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys Lys Pro	
485 490 495	
GCA CTG GAC AAG GGC CTG GGC ACC GGC CAG GGT GCA GTG TCA GGA CCC	1652
Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser Gly Pro	
500 505 510	
CCC CGG AAG CCT CCT GGG ACT GTC GCT GGC ACA GCC CGA GGC CCT GAA	1700
Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly Pro Glu	
515 520 525 530	
GGT GGC AGC ACG GCT CAG GTG CCA GCA CCC GCA GCA TCA CCA CCG CCG	1748
Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro Pro Pro	
535 540 545	
GAG GGT CCA GTG CTC ACT TTC CAG AGT GAG AAG ATG AAG GGC ATG AAG	1796
Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly Met Lys	
550 555 560	
GAG CTG CTG GTG GCC ACC AAG ATC AAC TCG AGC GCC ATC AAG CTG CAA	1844
Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys Leu Gln	
565 570 575	
CTC ACG GCA CAG TCG CAA GTG CAG ATG AAG AAG CAG AAA GTG TCC ACC	1892
Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val Ser Thr	
580 585 590	
CCT AGT GAC TAC ACT CTG TCT TTC CTC AAG CGG CAG CGC AAA GGC CTC	1940
Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys Gly Leu	
595 600 605 610	
TGAACTACTG GGGACTTCGG ACCGCTTGTTG GGGACCCAGG CTCCGCCTTA GTCCCCAAC	2000
TCTGAGCCCA TGTTCTGCCC CCAGCCCCAA GGGGACAGGC CTCACCTCTA CCCAAACCCT	2060
AGGTTCCCCG TCCCGAGTAC AGTCTGTATC AAACCCACGA TTTTCTCCAG CTCAGAACCC	2120
AGGGCTCTGC CCCAGTCGTT AGAATATAGG TCTCTTCTCC CAGAATCCCA GCCGGCCAAT	2180
GGAAACCTCA CGCTGGGTCC TAATTACCAG TCTTTAAAGG CCCAGCCCCT AGAAACCCAA	2240
GCTCCTCCTC GGAACCGCTC ACCTAGAGCC AGACCAACGT TACTCAGGGC TCCTCCCAGC	2300
TTGTAGGAGC TGAGGTTTCA CCCTTAACCC AAGGGAGCAC AGGTCCCACC TCCAGCCCGG	2360
GGAGCCTAGG ACCACTCAGC CCCTAGGAGT ATATTTCCGC ACTTCAGAAT TCCATATCTT	2420
GCGAATCCAA GCTCCCTGCC CCAAATAACT TCAGTCCTGC TTCCAGAATT TGGAATCCT	2480
AGTTTCCTCT CCTTCGTATC CCGAGTCTGG GACACAAAAC TCCGCCCCCA GCCTATGAGC	2540
ATCCTGAGCC CCGCCCTCTT CTGACGAAA CTGGCCCCGG ATCAGAGCAG GACCTCCCTT	2600
CCGACCCTCT GGGAACCTCC CAGAGGTCCA GCCCATCTCG GAGCATCCCG GAGGAAATCT	2660
GCAGAGGGGT TAGGAGTGGG TGACAAGAGC CTGATCTCTT CCTGTTTGT ACATAGATTT	2720

ATTTTTCAGT TCCAAGAAAG ATGAATACAT TTTGTTAAAA AAAAAAAAAA AA

2772

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile  
1 5 10 15

Asp Asp Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro  
20 25 30

Asp Leu Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu  
35 40 45

Ala Val Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln  
50 55 60

Pro Ser Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val  
65 70 75 80

Ala Asp Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln  
85 90 95

Ile Arg Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val  
100 105 110

Ser Ser Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser  
115 120 125

Leu Ser Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe  
130 135 140

Ser Phe Ile Thr Gly Thr Lys Leu Asp Ser Ser Gly Val Ala Phe Ala  
145 150 155 160

Val Val Gly Ala Cys Gln Ala Leu Gly Leu Arg Asp Val His Leu Ala  
165 170 175

Leu Ser Glu Asp His Ala Trp Val Val Phe Gly Pro Asn Gly Glu Gln  
180 185 190

Thr Ala Glu Val Thr Trp His Gly Lys Gly Asn Glu Asp Arg Arg Gly  
195 200 205

Gln Thr Val Asn Ala Gly Val Ala Glu Arg Ser Trp Leu Tyr Leu Lys  
210 215 220

Gly Ser Tyr Met Arg Cys Asp Arg Lys Met Glu Val Ala Phe Met Val  
225 230 235 240

Cys Ala Ile Asn Pro Ser Ile Asp Leu His Thr Asp Ser Leu Glu Leu  
245 250 255

Leu Gln Leu Gln Gln Lys Leu Leu Trp Leu Leu Tyr Asp Leu Gly His  
 260 265 270  
 Leu Glu Arg Tyr Pro Met Ala Leu Gly Asn Leu Ala Asp Leu Glu Glu  
 275 280 285  
 Leu Glu Pro Thr Pro Gly Arg Pro Asp Pro Leu Thr Leu Tyr His Lys  
 290 295 300  
 Gly Ile Ala Ser Ala Lys Thr Tyr Tyr Arg Asp Glu His Ile Tyr Pro  
 305 310 315 320  
 Tyr Met Tyr Leu Ala Gly Tyr His Cys Arg Asn Arg Asn Val Arg Glu  
 325 330 335  
 Ala Leu Gln Ala Trp Ala Asp Thr Ala Thr Val Ile Gln Asp Tyr Asn  
 340 345 350  
 Tyr Cys Arg Glu Asp Glu Glu Ile Tyr Lys Glu Phe Phe Glu Val Ala  
 355 360 365  
 Asn Asp Val Ile Pro Asn Leu Leu Lys Glu Ala Ala Ser Leu Leu Glu  
 370 375 380  
 Ala Gly Glu Glu Arg Pro Gly Glu Gln Ser Gln Gly Thr Gln Ser Gln  
 385 390 395 400  
 Gly Ser Ala Leu Gln Asp Pro Glu Cys Phe Ala His Leu Leu Arg Phe  
 405 410 415  
 Tyr Asp Gly Ile Cys Lys Trp Glu Glu Gly Ser Pro Thr Pro Val Leu  
 420 425 430  
 His Val Gly Trp Ala Thr Phe Leu Val Gln Ser Leu Gly Arg Phe Glu  
 435 440 445  
 Gly Gln Val Arg Gln Lys Val Arg Ile Val Ser Arg Glu Ala Glu Ala  
 450 455 460  
 Ala Glu Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg  
 465 470 475 480  
 Arg Gly Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys  
 485 490 495  
 Lys Pro Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser  
 500 505 510  
 Gly Pro Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly  
 515 520 525  
 Pro Glu Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro  
 530 535 540  
 Pro Pro Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly  
 545 550 555 560  
 Met Lys Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys  
 565 570 575

Leu Gln Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val  
                   580                                  585                                  590  
 Ser Thr Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys  
                   595                                  600                                  605  
 Gly Leu  
           610

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..9180
- (D) OTHER INFORMATION: /note= "genomic sequence for MEN1 gene"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1680..1766

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1767..2264

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 2265..2732

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2733..4296

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4297..4505

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4506..4715

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4716..4844

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4845..5176

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 5177..5217



(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 5218..5297

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 5298..5385

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 5386..6024

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 6025..6161

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 6162..6622

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 6623..6758

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 6759..7195

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 7196..7360

(ix) FEATURE:  
 (A) NAME/KEY: intron  
 (B) LOCATION: 7361..7577

(ix) FEATURE:  
 (A) NAME/KEY: exon  
 (B) LOCATION: 7578..8881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGTCTTGA ACTCCTGGCC TCAAGCAATC CTCCTGCTTC AGCTTCCCAA AGTGTTGTAA	60
TTACAGGCAT GAGCCTGGCA TGAAGTTGAC ACTATTGAGA TATACTGGTC AGGTATTTTG	120
TGGAATGTCC CTCAACTCTG TTTTGCCAGA TGTTTTCTCA TGATTAGAGG AGAGTTATAA	180
ATTTTGAGGA AAATCCAGAG AGGTGAAGAG GTGAAGTAGG GCAGAAATTT AATCTGTTTT	240
ATTTACTGCT ATATACCGAG TGTCTGGAAC TTGGCCCATG GTAAGTACCA AAAATCTGTT	300
TTTTTTGAAT GAATAAGCAA ATAAATGAGT GACCGTGGAA ATTTAGTATT ATTTCAAAGT	360
TTCAAAGCGT TGTTGATACA GGCCAGGCAC AGTGGCTCAC ACCTGTAATC CCAGCACTTT	420
TGGAGGCCGA GGTAGGAGGA TCACTTGAGG TCAGGAGTTC GAGACCAGCC TGACCAACAT	480
GGTGACACCC CTGTCTCTAC TAAGTAAAT ACAAAAATTA GCCAAGTGTG GTGGCAGGCA	540

CCTGTAATCC CGGCTACTTG GGAAGCTGAG GCAGAAGAAT CACTTGAACC TGGGAGGCAG 600  
 AGGTTGCAGT GAGCCGAGAT CACCCCACTG CACTCCAGCC TGAGTGACAG AGCGAGACTC 660  
 TGTCTCAAAA CAAATAAACA AATAACTACT CTTTGGCCGG GTAAGGTGGT TCACGCCTGT 720  
 AATTTTAGCA CTTTGGGAGG CTGAGGCGGG CAGATCACTT GAGGTTAGGG GTTCGAGACC 780  
 AGTCTGGCCA ACATGGTGAA ACCCCATCTC TACTTAAAAT AAAAAAGTT TTCTGGGTGT 840  
 GGTGGCGGAC GCCTATAATC CCAGCTACTT GGGACTTTTT TTTAAGACGG AATCTCACTC 900  
 TGTGCCCAG GCTGGAGTGC AGTGGCAAGA TTCTGGCTCA CTGAAGCCTC CGCCTCCCAG 960  
 GTTCAAGGGG ATTCCCCGCG CCTCAGCCTC CCAAGTAGCT GGGAATCCCT GTCTCTGCAA 1020  
 AAAAAAAAAA AAAAAAAAAAC AAAAAATATA TATATATATA TATATGTGTG TGTGTGTGTG 1080  
 TGTGTGTGTG TTATATGTAT ATATATTTAT GTATATGCAC ATACACACAA AATTAGGCGG 1140  
 GAGTGGTGGC GCACGCCTGT GATCACAGCT ACTCGGGAGG CTGAGGCACG AGAATCGCTT 1200  
 GAGCCCGTGA AGTCGAGGCT GCAGTGAGCC CAGATCGAGC CACTGCATTC CAGCCTGGGC 1260  
 GAAAGAGAAA GACCGTGTCT CAAAACAAAC AAACAAAAGC TACTCTTAGC ACGTGTTAGA 1320  
 GTATCTCGCG GGCGGAAGTG GGAAACGAGT GCTGCACACA GAGTAGGCAT CTTTATATGT 1380  
 TAACAGACAC TGATACCCAG CTAAAGCGGC TGAACACATT TACTCTCTGG CAGTGTTTAA 1440  
 AAGTATCTGT TTTTCTCATA TTGTTTTATT TTAATTTTTT CTGGATCAAG CAACCTGATC 1500  
 TTTTTCCTCA TAACTTGCCG ACCGACCCGT GACAGCAAAA CCGGCAGAAG CTCGGCGACC 1560  
 TCCCACCCCG AGTCTGCAGG TAGTGCCCCC GGACTACATT TTCCAGAAGG CACTGCGGGC 1620  
 ACGCTTCCTG CCTGGTCGGC CTGAAGGGAA GGGCCAATCC CTGAGTATCT CGGGAAGGAG 1680  
 GTGTCCGGAG CCGCGGACCT AGAGATCCCA GAAGCCACAG CGCAGCGGCC CGGCCCCGCA 1740  
 CTATTTCCAG GCTCTGCGGG GCAGGGGTGG GCCCAGACTC CACTTCCCGG CGGGTAGTGC 1800  
 GACCCTAGGG GCGGGACTTC ATGTCCCAGC AGGCTCCGGG CGGCGTGCAG CGCGGTGCCT 1860  
 AGTGTGGGAT GTAAGCGCGG AGGTGGGCGA GGGGGACCGA GGCCAGGACT CTCCTTGGGG 1920  
 TTTGGGGGCT TGACCTGGGT GCGCTTTCTG GACAGACTTT ACAGCCCCCG GGGGCACAGT 1980  
 CGTAGAGAGG GGGCGGGGCG GCCATTGGGG CTCCTCATTG GGGTGCTTGG GGCGCACCCC 2040  
 ATCGGGTACC GGGCGTCCCG GAATTGTGGG GGACAAAAG GCTCTGCAGT CTCGGCTGAG 2100  
 GGGTCTCACC GACAAAAGAG GGGAAGCCGG TGAGCAGAGG CTGAAGAGGG TGGGAAGCA 2160  
 GGGGAGCTGT GCGTGTGTCG GGGCGGGTGG AACCTTAGCG GACCCTGGGA GGAGGCTCCC 2220  
 CGGCCGAACC TGCCCGACCC TCCCTCCCCC GGCTTGCTT GCAGGCCGCC GCCACCGCC 2280  
 CGCCGCCATG GGGCTGAAGG CCGCCAGAA GACGCTGTTC CCGCTGCGCT CCATCGACGA 2340  
 CGTGGTGCGC CTGTTTGCTG CCGAGCTGGG CCGAGAGGAG CCGGACCTGG TGCTCCTTTC 2400

CTTGGTGCTG GGCTTCGTGG AGCATTTTCT GGCTGTCAAC CGCGTCATCC CTACCAACGT 2460  
 TCCCGAGCTC ACCTTCCAGC CCAGCCCCGC CCCCAGCCCG CCTGGCGGCC TCACCTACTT 2520  
 TCCCGTGGCC GACCTGTCTA TCATCGCCGC CCTCTATGCC CGCTTCACCG CCCAGATCCG 2580  
 AGGCGCCGTC GACCTGTCCC TCTATCCTCG AGAAGGGGGT GTCTCCAGCC GTGAGCTGGT 2640  
 GAAGAAGGTC TCCGATGTCA TATGGAACAG CCTCAGCCGC TCCTACTTCA AGGATCGGGC 2700  
 CCACATCCAG TCCCTCTTCA GCTTCATCAC AGGTTGGAGC CCAGTAGGTG GGAATCTTAT 2760  
 CCATGACCCA CTTCTTCAAA ACCCTCCATG GTTTACAGAA CCCTTTTAAG AACTGTAAGC 2820  
 CTTGTGAGGT TCGGCAGGTG TTATTTTCCT CTTTGCAGTT GGGAAACTGA AGCCCAGAGA 2880  
 GGGGAAATGA TATGCCAAAG TCACACACGG CATGGCAGGG CTGGAAGTGA AGCCTGATCA 2940  
 CTTGGCTCCA AATCATCAAC CTCACCTCTG CCCCCTCAGC ACCCCCACCC TTGCCACTGA 3000  
 ACAGCTACAG GAGTTCTAAG CATGAGACAC AGAGGGCGGC AGCAGATTTA GGGGGCAAGA 3060  
 AGATGAAATT GGGCTGCATT TGAGGCAGTT AAACAAAATA ATGGCTATGA AGATTTTTTT 3120  
 TTTTTTTTTT TTTTGAGACA GGGTCTCACT CTGTCCCCCA GGCTGGAGTG CAGTGGTGTG 3180  
 ATCATGGCTC ACTGCAGCCT CAGTCTCCCT GGGCTCAGAG ATCCTCCAAC CTCAGCCTCC 3240  
 TGAGTAGCTG AGAGTACAGG CATGCACCGT GGTGCTGGTT AATTTTTTGT ATTTTTTTTG 3300  
 TAGAGATGGT GTCTCACTAT GTGGCCCAGA CTGGTCTTGA ACTCTTGGGC TCAAGTGATC 3360  
 TGCCCGCTC AGTCTCCCAA ATGCTGGGAT TACAGGTGTG AGCCACCGCA ACTGGTGGCC 3420  
 TATGAAAATT TTTTTTTTTT TTCAGACGGC GTCTCACTCT GTCGCCCAGG CTGGAGTGCA 3480  
 GTGGTGCAAT CTCGGCTCAC TGCAAGCTCT GCCTCCTGCT TTCATGCCAT TCTCCTGCCT 3540  
 CCTGCCTCAG CCTCCTGAGT AGCTGGGACT ACAGGAGCCT GCCACCATGC CTGGCTAATT 3600  
 TTTTTTTGGA TTTTGTAGTAG AGACGAGGTT TCACCATGTT AGCCAGGATG GTCTCGATCT 3660  
 CCTGACCTCG TGATCCGCCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCGTGAGCC 3720  
 ACCGCACCTG GTCAAAAATG TTTGAGACAG AGAAGGGGCT TGACCTCAAA AGGCTTAAGA 3780  
 GTCAGGGCTT GCAAAGAGCT TTGCACCAAG CCCGTTGAC TGGCAATCCC ATCCTGGTGT 3840  
 GCCATATTGA GAAGGAATCA GAGGCTGCTT CTCAGCTTAG CAGGAAAAGA GTGCAGAGAT 3900  
 AAATGAGGGT TATTTGTTGG TGGGTGTATA GCCAGAGAGT GTTGGCCAGC GTCCTGT'TTT 3960  
 TGCCATTCCCT GTTTTAACCT AGTAAGTGCA GTAAAATGGA ATCCCTAAAT CCATAGAATA 4020  
 TATAATAGAG TTGCAGAGAA AGACGAGGTA GGGCCAAAGG CTGGGTCAGC TACAGGATAT 4080  
 CCAGAAAGGT ATCTTGTTGG ACATAGAGGG TGTAACACAG GAGAGAGTCT TTGAACACGT 4140  
 GGGAGGGAAG GGATGGAGGG ATAGTGGGCA GGAGAATCTG AGGTTGGGTC ACAGGCTTGG 4200  
 AAAGGGAGTG GGAGGGAGTG TGGCCCATCA CTACCTGGCC CCTTTCCCCA TGTAAAGCA 4260

CAGAGGACCC TCTTTCATTA CCTCCCCCTT CCACAGGCAC CAAATTGGAC AGCTCCGGTG 4320  
 TGGCCTTTGC TGTGGTTGGG GCCTGCCAGG CCCTGGGTCT CCGGGATGTC CACCTCGCCC 4380  
 TGTCTGAGGA TCATGCCTGG GTAGTGTTTG GGCCCAATGG GGAGCAGACA GCTGAGGTCA 4440  
 CCTGGCACGG CAAGGGCAAC GAGGACCGCA GGGGCCAGAC AGTCAATGCC GGTGTGGCTG 4500  
 AGCGGGTATT GTTCCCTCCC CCCAGCCTTG TCCCCTTCAT ACTGTAGTAG CCCAAGCCAC 4560  
 CCAAGGGACT CCATTTTCTT GGGCCACACC CCTTTCTTCC CATCACCACC CACATAGGAA 4620  
 GGAAGACAG AAGAGCCCCT TTTCTGGCT GTCATTCCCT GAAGCAGGCA CAGGGTGGGC 4680  
 CATCATGAGA CATAATGATC TCATCCCCC CTAAGAGCTG GCTGTACCTG AAAGGATCAT 4740  
 ACATGCGCTG TGACCGCAAG ATGGAGGTGG CGTTCATGGT GTGTGCCATC AACCTTCCA 4800  
 TTGACCTGCA CACCGACTCG CTGGAGCTTC TGCAGCTGCA GCAGGTGAGG GCTGAGCCAA 4860  
 TGGGGCAGGA CTGGGCTAGG CCAGACTTGA CTTGCTGTGG GACCTGGGC AGGGGCACTT 4920  
 TCCCTTCCTG AGCTTCAGCT TCCCCTCCTG GAAAAATGGG TTAGTAATTC CTGGCCTGGC 4980  
 CTTTCCAGG GCTCTTGGGA GAGTAGAATT GAGATGTGAA ATTGCTTTGA CTCCATTAAA 5040  
 GGGCTGGTCC CAGAATTTTG GCCCTTCCAC ATGGTGGGTG GTCCCTGTTG GTTCTGACCC 5100  
 CCACCTCTGC CCGATAGGCT AAGGACCGT TCTCCTCCCT GTTCCGTGGC TCATAACTCT 5160  
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 TTATGATCCT TTCTAGGTA CCCCATGGCC TTAGGGAACC TGGCAGATCT AGAGGAGCTG 5340  
 GAGCCCACCC CTGGCCGGCC AGACCCACTC ACCCTCTACC ACAAGGTGGG GGCATCTAAG 5400  
 GAGGGTGAG AAGGGAGACC CTAACAGTGG CTGAGGCAGG GGCCCTCATC TGGGCAGATG 5460  
 AGAAGAGAAC TTTGTGTGTT GGGGGGTATC GCCCATCCAG TCTCACTTTG TGTCAACTGT 5520  
 GTGCAGAAATC AGTTCAGTCA GGGCTGTCTG AGGGGTGTCC AGGGTTCCCC AGCCTGGGAG 5580  
 TGGCAGGGGC TGCATTTGTC CCCTCAGCCC TGCCTTTTCT GCCACTGCTT ACTGTCCTTC 5640  
 CTGGAGTATA ACAGAGGTCA AATGTGGTAG GAGCACTGAA GAGGGGGTGT TCACTTGGTG 5700  
 GGTGTAGGTG GGGAGGAGGG CCATTGGGCT GGGCTTGAAA GTCTTTGGTG ATGTGTAGAA 5760  
 GAGTGTCTGA GAAAGAGAAG GGCCCTGAGC TCGGAGGGCA GGCCCCACCC CTGCAGTCTG 5820  
 CCCCAGGCCT CAGCCAGCAG TCCTGTAGAC CCAGGGAGGA GACCAGGTAG AAGGGCTGGC 5880  
 AGCGAGTGGA GGTGGGAGTG GAGATGGAGA GGA CTCCCTG GGATCTTCCT GTGGCCCCTT 5940  
 CTGGGTGTGC CCTGGTGGGG CATTTGTGCC AGCAGGGCAG CTGGGGCTGC CTCCCTGAGG 6000  
 ATCCTCTGCC TCACCTCCAT CCAGGGCATT GCCTCAGCCA AGACCTACTA TCGGGATGAA 6060  
 CACATCTACC CCTACATGTA CCTGGCTGGC TACCACTGTC GCAACCGCAA TGTGCGGGAA 6120

GCCCTGCAGG CCTGGGCGGA CACGGCCACT GTCATCCAGG AGTGAGGATC CCCCTACTAG 6180  
 GGCCTGCAGC CTGTCCTTTC TTCCCCTCCA TCAGTTTCCA ACCACCCCTCG TCCAGGACTG 6240  
 AGGCCTGGCT CCCACGCCCC ATCCCCTTTC CATCCAGTCC CTAGGCAGCA AGGCCACCAT 6300  
 TACCCAGGAG GTAGGGACCC TGATTAAGGT GTCACATCTT TCCCTCCCTC CCCTCTCCTC 6360  
 CTAATTTTTT TTTTCTCAGA ACAGTCTCAA ATCTCCAATG TTTAACCACC ATCATCCAGC 6420  
 AGTGGGACTT CCACCCTCGG CCCCATGCCC CCCTCCTCAT TCTTGCTTTC TTCCTCTGGG 6480  
 CTGACCCAGA CAGCATCATT TTGCAGTGAG GACCCACCT ACTCCCCCAG CCCCTGGGGG 6540  
 CTCCATCCCC CGCCAGGTCC CTGGGGCTAC CCCCGATGGT GAGACCCCTT CAGACCCTAC 6600  
 AGAGACCCCA CTGCTCTCAC AGCTACAAC ACTGCCGGGA AGACGAGGAG ATCTACAAGG 6660  
 AGTTCTTTGA AGTAGCCAAT GATGTCATCC CCAACCTGCT GAAGGAGGCA GCCAGCTTGC 6720  
 TGGAGGCGGG CGAGGAGCGG CCGGGGGAGC AAAGCCAGGT GAAAGGCTGG AGCTCCAGCC 6780  
 TGTGTCCAGC CTCCCACCTG GACAGGGCTC CCTTCCACAG GGCCATGGGG GCTGCATGTA 6840  
 CGGGATTAGG GATGGCAGGA GGAAGGTGGC CCTGAGCAGA CAGCTATGTT CCCTTTTGCT 6900  
 ATAAGTGAAG TCCTGGGCCC ACGTTGGACG GGAAGTGAAG TATTTTAGAG GTTCTACCC 6960  
 TGTGCCTTCA GTTTCATGGC CAGACTCCCT CCCTCAGCTG AGGGGTGGAG GTAGGGATGG 7020  
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 TATGCTTACC TTTTCTGGAG CCAGGGGTCT TTGCCTAGGT GGGGGGCCTG GCCTGTGCCC 7140  
 TCTGCTAAGG GGTGAGTAAG AGACTGATCT GTGCCCTCCC TTCCCCCTCG TCCAGGGCAC 7200  
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 CGACGGCATC TGCAAATGGG AGGAGGGCAG TCCCACGCCT GTGCTGCACG TGGGCTGGGC 7320  
 CACCTTTCTT GTGCAGTCCC TAGGCCGTTT TGAGGGACAG GTGAGGGACA GCTGCACAGA 7380  
 GGTCTGGGCA CTACAGGTGG TGACAGCAGC CACGGGCTTG TCAGACTTTT CTGGCCCAGG 7440  
 GGCAGCATCT GCCCATCCCC TTCGGTGCCG ATGGGACTGA GACCCCTGG GTGGGATGGG 7500  
 ATGGCCAGAG CAGGGTCCTG GAGTTCAGC CACTGGCCGG CAACCTTGCT CTCACCTTGC 7560  
 TCTCCCCACT GGCCAGGTG CGGCAGAAGG TGCGCATAGT GAGCCGAGAG GCCGAGGCGG 7620  
 CCGAGGCCGA GGAGCCGTGG GGCAGGAAG CCCGGAAGG CCGGCGGCGG GGCCACGGC 7680  
 GGGAGTCCAA GCCAGAGGAG CCCCCGCCG CCAAGAAGCC AGCACTGGAC AAGGGCCTGG 7740  
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 CAGCCCGAGG CCCTGAAGGT GGCAGCACGG CTCAGGTGCC AGCACCCGCA GCATCACCAC 7860  
 CGCCGGAGGG TCCAGTGCTC ACTTTCCAGA GTGAGAAGAT GAAGGGCATG AAGGAGCTGC 7920  
 TGGTGGCCAC CAAGATCAAC TCGAGCGCCA TCAAGCTGCA ACTCACGGCA CAGTCGCAAG 7980

TGCAGATGAA GAAGCAGAAA GTGTCCACCC CTAGTGA CACTCTGTCT TTCCTCAAGC 8040  
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 CGCCTTAGTC CCCCAACTCT GAGCCCATGT TCTGCCCCCA GCCCAAAGGG GACAGGCCTC 8160  
 ACCTCTACCC AAACCCTAGG TTCCCGGTCC CGAGTACAGT CTGTATCAAA CCCACGATTT 8220  
 TCTCCAGCTC AGAACCCAGG GCTCTGCCCC AGTCGTTAGA ATATAGGTCT CTTCTCCCAG 8280  
 AATCCCAGCC GGCCAATGGA AACCTCACGC TGGGTCCTAA TTACCAGTCT TTAAAGGCCC 8340  
 AGCCCCTAGA AACCCAAGCT CCTCCTCGGA ACCGCTCACC TAGAGCCAGA CCAACGTTAC 8400  
 TCAGGGCTCC TCCAGCTTG TAGGAGCTGA GGTTCACCC TTAACCCAAG GGAGCACAGG 8460  
 TCCCACCTCC AGCCCGGGGA GCCTAGGACC ACTCAGCCCC TAGGAGTATA TTTCCGCACT 8520  
 TCAGAATTCC ATATCTTGCG AATCCAAGCT CCCTGCCCCA AATAACTTCA GTCCTGCTTC 8580  
 CAGAATTTGG AAATCCTAGT TTCCTCTCCT TCGTATCCCG AGTCTGGGAC ACAAACCTCC 8640  
 GCCCCCAGCC TATGAGCATC CTGAGCCCCG CCCTCTTCCT GACGAAACTG GCCCCGGATC 8700  
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 CATCCCGGAG GAAATCTGCA GAGGGGTTAG GAGTGGGTGA CAAGAGCCTG ATCTCTTCCT 8820  
 GTTTTGTACA TAGATTTATT TTTCAGTTCC AAGAAAGATG AATACATTTT GTTAAAAAAA 8880  
 ATATAAAGCG CAAGTCCATG TTTATCTGGG AAATTGGGGA TGGGGCGGGG AGTGGAGCGC 8940  
 CCCTTCTTCC CTTTGTCTTC TGGCTCCCGG GACTTTGCGC TCCCTACCTG TGGAGCGCGA 9000  
 GCGACAGTGG CGGCGGAAGG ACGTAGGCTC CGCCCCGGCC TTGGGGCTTC CCCC GCGCCG 9060  
 CCGAGGGCCC GTCCCGCGGG CGCCTCCTCC CGGACTGGCG GTGGGGCATC CCNNGGCGCG 9120  
 GCCCCGCCCC CGGGCTTCAG CCCC GCCCCC GCGGCTTCAG AGCCACGGGC GCCCGCCCCG 9180

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "antisense strand from patient with 512delC frameshift mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCTTAAG TAGGAGCGG

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 500-519 of MEN1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCTTGAA GTAGGAGCGG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 1405-1424 of MEN1 cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCCCAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from position  
1417 C->T substitution, resulting in  
W436X mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGGCCTAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACCTGGGTG CGCTTTCTGG AC

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTGGACATA GAGGGTGTAACACAG

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGAGCTCG GGAACGTTGG TAG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGACCTTCT TCACCAGCTC ACGG

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAACCTCAC AAGGCTTACA GTTC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTGGACATA GAGGGTGTAACACAG

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACAGTTGACA CAAAGTGAGA CTGG

24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCTTCTG TCTTCCTTC CTATG

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCCACAG CAAGTCAAGT CTGG

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGTTCCGT GGCTCATAAC TCTC

24

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTCAGCCAG CAGTCCTGTA GA

22

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAGGGT GGTGGAAC TG

22

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGACTCCTTG GGATCTTCCT GTG

23

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AACGACCATC ATCCAGCAGT GG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCATCCCTAA TCCCGTACAT GC

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGTGAGACC CCTTCAGACC CTAC

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGCTAAGGG GTGAGTAAGA GAC

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGATAC AGACTGTACT CGG

23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCTGACAAG CCCGTGGCTG CTG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCATCTGCCC ATCCCCTTCG GTG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAAGCCTCCT GGGACTGTCG CTG

23